```
     AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGGATTTTGGGCTGATTTTTTTTA
   1 ---------+---------+---------+---------+---------+---------+  60
     TTCGAAATGTCAATGAGTCGTGTGTCCTGGAGTGGTACCTAAAACCCGACTAAAAAAAAT

C      A  L  Q  L  L  S  T  Q  D  L  T  M  D  F  G  L  I  F  F  I   -


     TTGTTCTTTTAAAAGGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGG
  61 ---------+---------+---------+---------+---------+---------+  120
     AACAAGAAAATTTTCCCCAGGTCTCACTTCACTTCGAACTCCTCAGACCTCCTCCGAACC

C      V  L  L  K  G  V  Q  S  E  V  K  L  E  E  S  G  G  G  L  V   -


     TGCAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTTACTTTCAGTGGCT
 121 ---------+---------+---------+---------+---------+---------+  180
     ACGTTGGACCTCCTAGGTACTTTGAGAGGACACATCGGAGACCTAAATGAAAGTCACCGA

C      Q  P  G  G  S  M  K  L  S  C  V  A  S  G  F  T  F  S  G  Y   -


     ACTGGATGTCTTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTA
 181 ---------+---------+---------+---------+---------+---------+  240
     TGACCTACAGAACCCAGGCGGTCAGAGGTCTCTTCCCCGAACTCACCCAACGACTTTAAT

C      W  M  S  W  V  R  Q  S  P  E  K  G  L  E  W  V  A  E  I  R   -


     GATTGAAATCTGATAATTATGCAACACATTATGCGGAGTCTGTGAAAGGGAAGTTCACCA
 241 ---------+---------+---------+---------+---------+---------+  300
     CTAACTTTAGACTATTAATACGTTGTGTAATACGCCTCAGACACTTTCCCTTCAAGTGGT

C      L  K  S  D  N  Y  A  T  H  Y  A  E  S  V  K  G  K  F  T  I   -


     TCTCAAGAGATGATTCCAAAAGTCGTCTCTACCTGCAAATGAACAGCTTAAGAGCTGAAG
 301 ---------+---------+---------+---------+---------+---------+  360
     AGAGTTCTCTACTAAGGTTTTCAGCAGAGATGGACGTTTACTTGTCGAATTCTCGACTTC

C      S  R  D  D  S  K  S  R  L  Y  L  Q  M  N  S  L  R  A  E  D   -


     ACAGTGGAGTTTATTACTGTACAGATTTCATAGACTGGGGCCAAGGGACACTAGT
 361 ---------+---------+---------+---------+---------+-----  415
     TGTCACCTCAAATAATGACATGTCTAAAGTATCTGACCCCGGTTCCCTGTGATCA

C      S  G  V  Y  Y  C  T  D  F  I  D  W  G  Q  G  T  L    -
```

FIG. 1

```
    AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGG
  1 ---------+---------+---------+---------+---------+---------+  60
    TTCGAAATGTCAATGAGTCGTGTGTCCTGGAGTGGTACTCCAAGAGACAAGTCAAAGACC

  C    A   L   Q   L   L   S   T   Q   D   L   T   M   R   F   S   V   Q   F   L   G  -


    GGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAAC
 61 ---------+---------+---------+---------+---------+---------+  120
    CCCACGAATACAAGACCTAGAGACCTCAGTCACCCCTATAACACTATTGGGTCCTACTTG

  C    V   L   M   F   W   I   S   G   V   S   G   D   I   V   I   T   Q   D   E   L  -


    TCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCTAGTAAGAGTC
121 ---------+---------+---------+---------+---------+---------+  180
    AGAGGTTAGGACAGTGAAGACCTCTTAGTCAAAGGTAGAGGACGTCCAGATCATTCTCAG

  C    S   N   P   V   T   S   G   E   S   V   S   I   S   C   R   S   S   K   S   L  -


    TCCTGTATAAGGATGGGAAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTC
181 ---------+---------+---------+---------+---------+---------+  240
    AGGACATATTCCTACCCTTCTGTATGAACTTAACCAAAGACGTCTCTGGTCCTGTTAGAG

  C    L   Y   K   D   G   K   T   Y   L   N   W   F   L   Q   R   P   G   Q   S   P  -


    CTCAGCTCCTGATGTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG
241 ---------+---------+---------+---------+---------+---------+  300
    GAGTCGAGGACTACATAAACTACAGGTGGGCACGTAGTCCTCAGAGTCTGGCCAAATCAC

  C    Q   L   L   M   Y   L   M   S   T   R   A   S   G   V   S   D   R   F   S   G  -


    GCAGTGGGTCAGGCACAGATTTCACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGG
301 ---------+---------+---------+---------+---------+---------+  360
    CGTCACCCAGTCCGTGTCTAAAGTGGGACCTTTAGTCATCTCACTTCCGACTCCTACACC

  C    S   G   S   G   T   D   F   T   L   E   I   S   R   V   K   A   E   D   V   G  -


    GTGTGTATTACTGTCAACAACTTGTAGAGTATCCATTCACGTTCGGCTCGGGGACAAAGT
361 ---------+---------+---------+---------+---------+---------+  420
    CACACATAATGACAGTTGTTGAACATCTCATAGGTAAGTGCAAGCCGAGCCCCTGTTTCA

  C    V   Y   Y   C   Q   Q   L   V   E   Y   P   F   T   F   G   S   G   T   K   L  -


    TGGAAATAAAACGTACG
421 ----------------  437
    ACCTTTATTTTGCATGC

  C    E   I   K   R   T  -
```

FIG. 2

09/674716

```
         GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
      1  ---------+---------+---------+---------+---------+---------+  60
         CTATAACACTACTGAGTCAGAGGTGAGAGGGACGGGCAGTGGGGACCTCTCGGCCGGAGG
                            FRI
      A  [D  I  V  M  T  Q  S  P  L  S  L  P  V  T  P  G  E  P  A  S  -
                  69|70                                      117|118
         ATCTCCTGT CGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATGG
     61  ---------+---------+---------+---------+---------+-------+--+  120
         TAGAGGACA GCGAGCTCATTCTCAGAGGACATATTCCTACCCTTCTGTATGAACTTAACC
                                                  CDRI
      A  I  S  C] [R  S  S  K  S  L  L  Y  K  D  G  K  T  Y  L  N] [W  -
                                               162|163
         TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA
    121  ---------+---------+---------+---------+-+-------+---------+  180
         ATGGACGTCTTCGGTCCCGTCAGAGGTGTCGAGGACTAGATAAACTACAGGTGGGCCCGT
                        FR2                              CDR2
      A  Y  L  Q  K  P  G  Q  S  P  Q  L  L  I  Y] [L  M  S  T  R  A  -
         183|184
         TCA GGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
    181  --+------+---------+---------+---------+---------+---------+  240
         AGT CCCCAGGGACTGTCCAAGTCACCGTCACCTAGTCCGTGTCTAAAATGTGACTTTTAG
                                        FR3
      A  S] [G  V  P  D  R  F  S  G  S  G  S  G  T  D  F  T  L  K  I  -
                                            279|280
         AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGT CAACAGCTGGTAGAGTATCCA
    241  ---------+---------+---------+---------+-+-------+---------+  300
         TCGTCTCACCTCCGACTCCTACAACCCCAAATAATGACA GTTGTCGACCATCTCATAGGT
                                                         CDR3
      A  S  R  V  E  A  E  D  V  G  V  Y  Y  C] [Q  Q  L  V  E  Y  P  -
            306|307                              339 [340
         TTCACG TTCGGCCAAGGGACCAAGGTGGAGATCAAACGT ACGGTGGCT
    301  ---+--+---------+---------+---------+-------- 348
         AAGTGC AAGCCGGTTCCCTGGTTCCACCTCTAGTTTGCA TGCCACCGA
                        FR4
      A  F  T] [F  G  Q  G  T  K  V  E  I  K  R] T  V  A  -
```
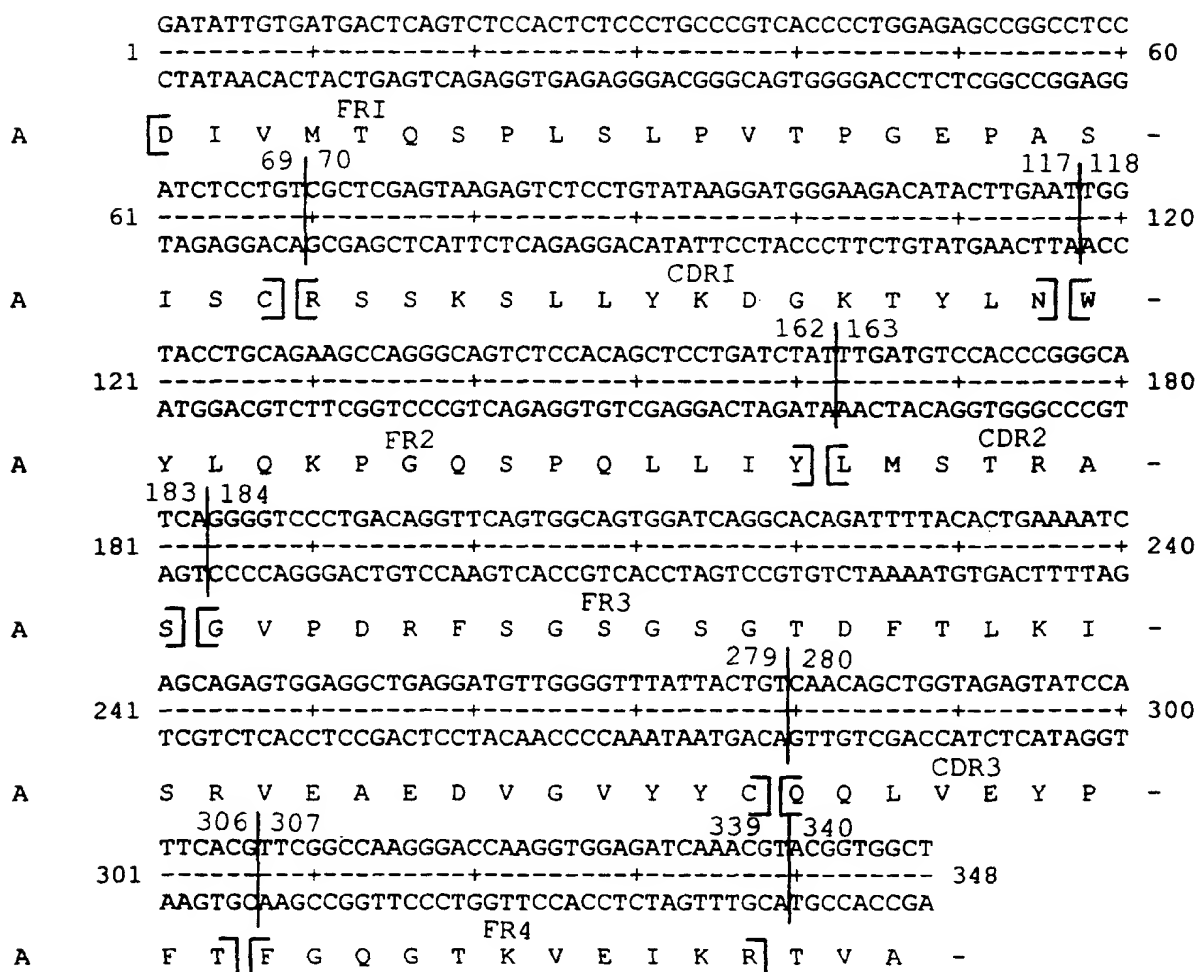
FIG. 3

4/6
FIG. 4

```
      GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTC
   1  ---------+---------+---------+---------+---------+---------+  60
      CTCCACGTCGACCACCTCAGACCCCCTCCGAACCATTTCGGGCCCCCCAGGGAATCTGAG
                                    FR1
A     [E  V  Q  L  V  E  S  G  G  G  L  V  K  P  G  G  S  L  R  L  -
                               90 91      105 106
      TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT
  61  ---------+---------+---------+---------+---------+---------+  120
      AGGACACGTCGATCGCCTAAGTGAAAGTCACCGATGACCTACAGGACCCAGGCGGTCCGA
                                         CDR1
A      S  C  A  A  S  G  F  T  F  S [G  Y  W  M  S][W  V  R  Q  A  -
                              147 148
      CCAGGGAAGGGGCTCGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA
 121  ---------+---------+---------+---------+---------+---------+  180
      GGTCCCTTCCCCGAGCTCACCCAACGACTTTAATCTAACTTTAGACTATTAATACGTTGT
              FR2                                       CDR2
A      P  G  K  G  L  E  W  V  A][E  I  R  L  K  S  D  N  Y  A  T  -
                             204 205
      CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA
 181  ---------+---------+---------+---------+---------+---------+  240
      GTAATACGCCTCAGACACTTCCCCTTTAAGTGGTAGAGTTCTCTACTAAGTTTTAGATCT
A      H  Y  A  E  S  V  K ·G][K  F  T  I  S  R  D  D  S  K  S  R  -

      CTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACAGAT
 241  ---------+---------+---------+---------+---------+---------+  300
      GACATAGACGTTTACTTGTCGGACTTTTGGCTCCTGTGTCGGCACATAATGACATGTCTA
                             FR3
A      L  Y  L  Q  M  N  S  L  K  T  E  D  T  A  V  Y  Y  C  T  D] -
 300  301 309 310                      333
      TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCA
 301  ---------+---------+---------+---------+---------+---------+  360
      AAGTATCTGACCCCGGTCCCTTGTGATCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGT
          CDR3           FR4              CONSTANT REGION
A     [F  I  D][W  G  Q  G  T  L  V  T][V  S  S  A  S  T  K  G  P  -

      TCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGC
 361  ---------+---------+---------+---------+---------+---------+  420
      AGCCAGAAGGGGGACCGTGGGAGGAGGTTCTCGTGGAGACCCCCGTGTCGCCGGGACCCG
A      S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  -

      TGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTG
 421  ---------+---------+---------+---------+---------+---------+  480
      ACGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGTCCGCGGGAC
A      C  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L  -

      ACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
 481  ---------+---------+---------+---------+---------+---------+  540
      TGGTCGCCGCACGTGTGGAAGGGCCGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCG
A      T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L  S  -

      AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
 541  ---------+---------+---------+---------+---------+---------+  600
      TCGCACCACTGGCACGGGAGGTCGTCGAACCCGTGGGTCTGGATGTAGACGTTGCACTTA
A      S  V  V  T  V  P  S  S  S  L  G ·T  Q  T  Y  I  C  N  V  N  -

      CACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTGGAGCCCAAATCTTGTGACAAAACT
 601  ---------+---------+---------+---------+---------+---------+  660
      GTGTTCGGGTCGTTGTGGTTCCACCTGTTCTTTCACCTCGGGTTTAGAACACTGTTTTGA
A      H  K  P  S  N  T  K  V  D  K  K  V  E  P  K  S  C  D  K  T  -

      CACACATGCCCACCGTGCCCAGCACCTGAACTCGCGGGGGGCACCGTCAGTCTTCCTCTTC
 661  ---------+---------+---------+---------+---------+---------+  720
```
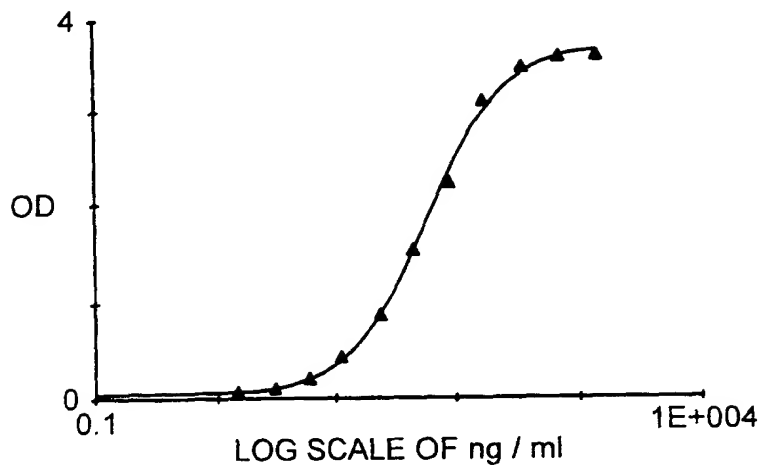
```
                GTGTGTACGGGTGGCACGGGTCGTGGACTTGAGCGCCCCCGTGGCAGTCAGAAGGAGAAG
      A           H   T   C   P   P   C   P   A   P   E   L   A   G   A   P   S   V   F   L   F   -

                CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTG
      721       ---------+---------+---------+---------+---------+---------+  780
                GGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCAC
      A           P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   V   T   C   V   V   -

                GTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
      781       ---------+---------+---------+---------+---------+---------+  840
                CACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTC
      A           V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   -

                GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
      841       ---------+---------+---------+---------+---------+---------+  900
                CACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAG
      A           V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   -

                AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC
      901       ---------+---------+---------+---------+---------+---------+  960
                TCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAG
      A           S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K   V   -

                TCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
      961       ---------+---------+---------+---------+---------+---------+  1020
                AGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGG
      A           S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   A   K   G   Q   P   -

                CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTC
      1021      ---------+---------+---------+---------+---------+---------+  1080
                GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAG
      A           R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   T   K   N   Q   V   -

                AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGC
      1081      ---------+---------+---------+---------+---------+---------+  1140
                TCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCG
      A           S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   V   E   W   E   S   -

                AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
      1141      ---------+---------+---------+---------+---------+---------+  1200
                TTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGG
      A           N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   D   S   D   G   S   -

                TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
      1201      ---------+---------+---------+---------+---------+---------+  1260
                AAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAG
      A           F   F   L   Y   S   K   L   T   V   D   K   S   R   W   Q   Q   G   N   V   F   -

                TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
      1261      ---------+---------+---------+---------+---------+---------+  1320
                AGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC
      A           S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   K   S   L   S   L   -

                TCTCCGGGTAAATGA
      1321      ---------+----- 1335
                AGAGGCCCATTTACT
      A           S   P   G   K   *   -
```

FIG. 4 CONT'D

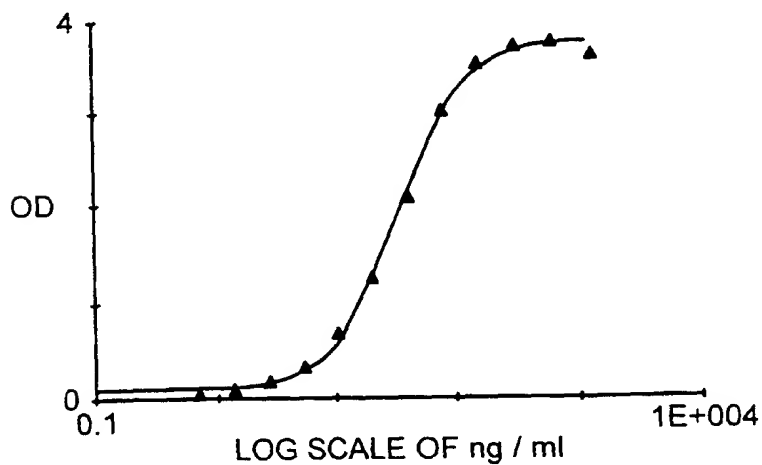6 / 6

$y=(A-D)/(1+(x/C)^B)+D$
A=0.0501 B=1.31 C=60.3 D=3.74

CHIMERIC CD23 IgG1m
HALF MAXIMUM BINDING=16.28ng/ml

FIG. 5

$y=(A-D)/(1+(x/C)^B)+D$
A=0.104 B=1.49 C=37.7 D=3.78

HUMANIZED CD23 IgG1m
HALF MAXIMUM BINDING=15.03ng/ml

FIG. 6